WHAT IS CLAIMED IS:

1)   A computer based method for evaluating information concerning candidate genes and experiments used to identify said candidate genes, wherein said candidate

5   genes are identified via examining expression levels of a plurality of genes, wherein said expression levels are measured by conducting hybridization experiments with nucleic acid microarray chips, said method comprising:

collecting a plurality of sample attributes from said experiments;

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collecting a plurality of study attributes from said experiments;

collecting a plurality of control attributes from said experiments;

15   collecting a plurality of data attributes from said experiments;

collecting a plurality of false positive/negative attributes from said experiments;

collecting a plurality of literature attributes concerning said candidate genes;

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collecting a plurality of patient attributes concerning said candidate genes;

collecting a plurality of clinical information attributes concerning said candidate genes;

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collecting a plurality of validation attributes concerning said candidate genes;

collecting a plurality of functional attributes concerning said candidate genes;

30   defining at least one of a plurality of groupings of said attributes;

selecting, based upon said at least one of a plurality of groupings, information about said plurality of attributes to be evaluated;

forming a plurality of resulting information;

5   and formatting said plurality of resulting information for viewing by a user.

2)   A computer based method according to claim 1 wherein said plurality of sample attributes are selected from the group consisting of sample quality data, sample matching information, total sample number information, and sample selection

10   criterion.

3)   A computer based method according to claim 1 wherein said plurality of study attributes are selected from the group consisting of the goal of the study, medical question addressed by the study, and known weaknesses of any model system

15   employed in the study.

4)   A computer based method according to claim 1 wherein said plurality of control attributes is selected from the group consisting of normalizing controls and baseline controls.

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5)   A computer based method according to claim 1 wherein said plurality of data attributes is selected from the group consisting of data filtration information, statistical methods employed in the analysis, including how statistical significance was determined and what thresholds were used, and range of expression level

25   observed for the candidate genes.

6)   A computer based method according to claim 1 wherein said plurality of false positive/negative attributes is selected from the group consisting of information on false positive management and information on false negative management.

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7)   A computer based method according to claim 1 wherein said nucleic acid

microarray chip is an oligonucleotide microarray chip.

8)   A computer program product for evaluating information concerning candidate genes and experiments used to identify said candidate genes, wherein said candidate genes are identified via examining expression levels of a plurality of genes, wherein said expression levels are measured by conducting hybridization experiments with nucleic acid microarray chips, said computer program product comprising:

code for collecting a plurality of sample attributes from said experiments;

code for collecting a plurality of study attributes from said experiments;

code for collecting a plurality of control attributes from said experiments;

code for collecting a plurality of data attributes from said experiments;

code for collecting a plurality of false positive/negative attributes from said experiments;

code for collecting a plurality of literature attributes concerning said candidate genes;

code for collecting a plurality of patient attributes concerning said candidate genes;

code for collecting a plurality of clinical information attributes concerning said candidate genes;

code for collecting a plurality of validation attributes concerning said candidate genes;

code for collecting a plurality of functional attributes concerning said candidate genes;

code for defining at least one of a plurality of groupings of said attributes;

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code for selecting, based upon said at least one of a plurality of groupings, information about said plurality of attributes to be evaluated;

code for forming a plurality of resulting information;

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and code for formatting said plurality of resulting information for viewing by a user.

9)   The computer program product of claim 8 wherein said plurality of sample
15   attributes is selected from the group consisting of sample quality data, sample matching information, total sample number information, and sample selection criterion.

10)   The computer program product of claim 8 wherein said plurality of study
20   attributions is selected from the group consisting of the goal of the study, medical question addressed by the study, and known weaknesses of any model system employed in the study.

11)   The computer program product of claim 8 wherein said plurality of control
25   attributes is selected from the group consisting of normalizing controls and baseline controls.

12)   The computer program product of claim 8 wherein said plurality of data attributes is selected from the group consisting of data filtration information, statistical
30   methods employed in the analysis, including how statistical significance was determined and what thresholds were used, and range of expression level

observed for the candidate genes.

13) The computer program product of claim 8 wherein said plurality of false positive/negative attributes is selected from the group consisting of information

5 on false positive management and information on false negative management.

14) The computer program product of claim 8 wherein said nucleic acid microarray chip is an oligonucleotide microarray chip.